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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/981,998DATE: 08/03/1999
TIME: 15:47:46

INPUT SET: S32762.raw #//

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: PULST, STEFAN M.

(ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
ATAXIA-2 AND PRODUCTS RELATED THERETO

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
(B) STREET: 119 NORTH FOURTH STREET, SUITE 203
(C) CITY: MINNEAPOLIS
(D) STATE: MINNESOTA
(E) COUNTRY: 55401
(F) ZIP: 55401

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/981,998
(B) FILING DATE: 11-MAY-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO 97/42314
(B) FILING DATE: 08-MAY-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/727,084
(B) FILING DATE: 08-OCT-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/022,207
(B) FILING DATE: 19-JUL-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/017,388
(B) FILING DATE: 08-MAY-1996

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47 (viii) ATTORNEY/AGENT INFORMATION:
48 (A) NAME: MUETING, ANN M.
49 (B) REGISTRATION NUMBER: 33,977
50 (C) REFERENCE/DOCKET NUMBER: 232.00010120
51
52 (ix) TELECOMMUNICATION INFORMATION:
53 (A) TELEPHONE: 612-305-1217
54 (B) TELEFAX: 612-305-1228
55
56
57 (2) INFORMATION FOR SEQ ID NO:1:
58
59 (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 516 base pairs
61 (B) TYPE: nucleic acid
62 (C) STRANDEDNESS: both
63 (D) TOPOLOGY: both
64
65 (ii) MOLECULE TYPE: DNA (genomic)
66
67
68
69
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
71
72 TTGGTAGCAA CGGAAACGGC GCGGGCGCGT TTCGGCCCCG CTCCCGGCGG CTCCTTGGTC 60
73
74 TCGGCGGGCC TCCCCGCCCC TTCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC 120
75
76 CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCC TGCGTCCCCG CCGCGTTCCG 180
77
78 GCGTCTCCTT GCGCGCCCCG GCTCCCGGCT GTCCCCGCCC GGCGTGCGAG CCGGTGTATG 240
79
80 GGCCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC 300
81
82 AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA 360
83
84 AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT 420
85
86 CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG 480
87
88 GGAGGCCCGG CCTGGGCAGG TGGGTGTCGG CACCCC 516
89
90 (2) INFORMATION FOR SEQ ID NO:2:
91
92 (i) SEQUENCE CHARACTERISTICS:
93 (A) LENGTH: 4481 base pairs
94 (B) TYPE: nucleic acid
95 (C) STRANDEDNESS: both
96 (D) TOPOLOGY: both
97
98 (ii) MOLECULE TYPE: cDNA
99

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100
101      (ix) FEATURE:
102          (A) NAME/KEY: CDS
103          (B) LOCATION: 163..4101
104
105
106      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
107
108      ACCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG      60
109
110      GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG      120
111
112      CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG      174
113                                     Met Arg Ser Ala
114                                     1
115
116
117      GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC      222
118      Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe
119      5              10              15              20
120
121      GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG      270
122      Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg
123      25              30              35
124
125      CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC      318
126      Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser
127      40              45              50
128
129      GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC      366
130      Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser
131      55              60              65
132
133      TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC      414
134      Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly
135      70              75              80
136
137      GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGC CCT      462
138      Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro
139      85              90              95              100
140
141      CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC      510
142      Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala
143      105              110              115
144
145      CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC      558
146      Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser
147      120              125              130
148
149      CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC      606
150      Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro
151      135              140              145
152

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153	CGC	CCG	GCG	TGC	GAG	CCG	GTG	TAT	GGG	CCC	CTC	ACC	ATG	TCG	CTG	AAG	654
154	Arg	Pro	Ala	Cys	Glu	Pro	Val	Tyr	Gly	Pro	Leu	Thr	Met	Ser	Leu	Lys	
155		150					155					160					
156																	
157	CCC	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CAA	CAG	CAG	CAG	CAG	CAA	CAG	702
158	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	
159	165						170				175					180	
160																	
161	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CCG	CCG	CCC	GCG	GCT	GCC	AAT	GTC	CGC	750
162	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala	Ala	Ala	Asn	Val	Arg	
163					185					190					195		
164																	
165	AAG	CCC	GGC	GGC	AGC	GGC	CTT	CTA	GCG	TCG	CCC	GCC	GCC	GCG	CCT	TCG	798
166	Lys	Pro	Gly	Gly	Ser	Gly	Leu	Leu	Ala	Ser	Pro	Ala	Ala	Ala	Pro	Ser	
167			200						205					210			
168																	
169	CCG	TCC	TCG	TCC	TCG	GTC	TCC	TCG	TCC	TCG	GCC	ACG	GCT	CCC	TCC	TCG	846
170	Pro	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Thr	Ala	Pro	Ser	Ser	
171			215					220					225				
172																	
173																	
174																	
175	GTG	GTC	GCG	GCG	ACC	TCC	GGC	GGC	GGG	AGG	CCC	GGC	CTG	GGC	AGA	GGT	894
176	Val	Val	Ala	Ala	Thr	Ser	Gly	Gly	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	
177		230					235					240					
178																	
179	CGA	AAC	AGT	AAC	AAA	GGA	CTG	CCT	CAG	TCT	ACG	ATT	TCT	TTT	GAT	GGA	942
180	Arg	Asn	Ser	Asn	Lys	Gly	Leu	Pro	Gln	Ser	Thr	Ile	Ser	Phe	Asp	Gly	
181	245					250					255					260	
182																	
183	ATC	TAT	GCA	AAT	ATG	AGG	ATG	GTT	CAT	ATA	CTT	ACA	TCA	GTT	GTT	GGC	990
184	Ile	Tyr	Ala	Asn	Met	Arg	Met	Val	His	Ile	Leu	Thr	Ser	Val	Val	Gly	
185					265					270					275		
186																	
187	TCC	AAA	TGT	GAA	GTA	CAA	GTG	AAA	AAT	GGA	GGT	ATA	TAT	GAA	GGA	GTT	1038
188	Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	Gly	Gly	Ile	Tyr	Glu	Gly	Val	
189			280					285					290				
190																	
191	TTT	AAA	ACT	TAC	AGT	CCG	AAG	TGT	GAT	TTG	GTA	CTT	GAT	GCC	GCA	CAT	1086
192	Phe	Lys	Thr	Tyr	Ser	Pro	Lys	Cys	Asp	Leu	Val	Leu	Asp	Ala	Ala	His	
193			295					300					305				
194																	
195	GAG	AAA	AGT	ACA	GAA	TCC	AGT	TCG	GGG	CCG	AAA	CGT	GAA	GAA	ATA	ATG	1134
196	Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly	Pro	Lys	Arg	Glu	Glu	Ile	Met	
197		310					315					320					
198																	
199	GAG	AGT	ATT	TTG	TTC	AAA	TGT	TCA	GAC	TTT	GTT	GTG	GTA	CAG	TTT	AAA	1182
200	Glu	Ser	Ile	Leu	Phe	Lys	Cys	Ser	Asp	Phe	Val	Val	Val	Gln	Phe	Lys	
201	325					330					335					340	
202																	
203	GAT	ATG	GAC	TCC	AGT	TAT	GCA	AAA	AGA	GAT	GCT	TTT	ACT	GAC	TCT	GCT	1230
204	Asp	Met	Asp	Ser	Ser	Tyr	Ala	Lys	Arg	Asp	Ala	Phe	Thr	Asp	Ser	Ala	
205					345					350					355		

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206																		
207	ATC	AGT	GCT	AAA	GTG	AAT	GGC	GAA	CAC	AAA	GAG	AAG	GAC	CTG	GAG	CCC		1278
208	Ile	Ser	Ala	Lys	Val	Asn	Gly	Glu	His	Lys	Glu	Lys	Asp	Leu	Glu	Pro		
209				360					365					370				
210																		
211	TGG	GAT	GCA	GGT	GAA	CTC	ACA	GCC	AAT	GAG	GAA	CTT	GAG	GCT	TTG	GAA		1326
212	Trp	Asp	Ala	Gly	Glu	Leu	Thr	Ala	Asn	Glu	Glu	Leu	Glu	Ala	Leu	Glu		
213			375					380					385					
214																		
215	AAT	GAC	GTA	TCT	AAT	GGA	TGG	GAT	CCC	AAT	GAT	ATG	TTT	CGA	TAT	AAT		1374
216	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn	Asp	Met	Phe	Arg	Tyr	Asn		
217		390					395					400						
218																		
219	GAA	GAA	AAT	TAT	GGT	GTA	GTG	TCT	ACG	TAT	GAT	AGC	AGT	TTA	TCT	TCG		1422
220	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr	Asp	Ser	Ser	Leu	Ser	Ser		
221	405					410					415					420		
222																		
223	TAT	ACA	GTG	CCC	TTA	GAA	AGA	GAT	AAC	TCA	GAA	GAA	TTT	TTA	AAA	CGG		1470
224	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	Glu	Glu	Phe	Leu	Lys	Arg		
225				425					430						435			
226																		
227	GAA	GCA	AGG	GCA	AAC	CAG	TTA	GCA	GAA	GAA	ATT	GAG	TCA	AGT	GCC	CAG		1518
228	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ile	Glu	Ser	Ser	Ala	Gln		
229				440					445					450				
230																		
231																		
232																		
233	TAC	AAA	GCT	CGA	GTG	GCC	CTG	GAA	AAT	GAT	GAT	AGG	AGT	GAG	GAA	GAA		1566
234	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp	Asp	Arg	Ser	Glu	Glu	Glu		
235			455					460					465					
236																		
237	AAA	TAC	ACA	GCA	GTT	CAG	AGA	AAT	TCC	AGT	GAA	CGT	GAG	GGG	CAC	AGC		1614
238	Lys	Tyr	Thr	Ala	Val	Gln	Arg	Asn	Ser	Ser	Glu	Arg	Glu	Gly	His	Ser		
239		470					475					480						
240																		
241	ATA	AAC	ACT	AGG	GAA	AAT	AAA	TAT	ATT	CCT	CCT	GGA	CAA	AGA	AAT	AGA		1662
242	Ile	Asn	Thr	Arg	Glu	Asn	Lys	Tyr	Ile	Pro	Pro	Gly	Gln	Arg	Asn	Arg		
243	485					490					495					500		
244																		
245	GAA	GTC	ATA	TCC	TGG	GGA	AGT	GGG	AGA	CAG	AAT	TCA	CCG	CGT	ATG	GGC		1710
246	Glu	Val	Ile	Ser	Trp	Gly	Ser	Gly	Arg	Gln	Asn	Ser	Pro	Arg	Met	Gly		
247					505					510					515			
248																		
249	CAG	CCT	GGA	TCG	GGC	TCC	ATG	CCA	TCA	AGA	TCC	ACT	TCT	CAC	ACT	TCA		1758
250	Gln	Pro	Gly	Ser	Gly	Ser	Met	Pro	Ser	Arg	Ser	Thr	Ser	His	Thr	Ser		
251				520					525					530				
252																		
253	GAT	TTC	AAC	CCG	AAT	TCT	GGT	TCA	GAC	CAA	AGA	GTA	GTT	AAT	GGA	GGT		1806
254	Asp	Phe	Asn	Pro	Asn	Ser	Gly	Ser	Asp	Gln	Arg	Val	Val	Asn	Gly	Gly		
255			535					540					545					
256																		
257	GTT	CCC	TGG	CCA	TCG	CCT	TGC	CCA	TCT	CCT	TCC	TCT	CGC	CCA	CCT	TCT		1854
258	Val	Pro	Trp	Pro	Ser	Pro	Cys	Pro	Ser	Pro	Ser	Ser	Arg	Pro	Pro	Ser		

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